

Changchuan Yin

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

1,687
citations

430874

18
h-index

345221

36
g-index

46
all docs

46
docs citations

46
times ranked

2370
citing authors

#	ARTICLE	IF	CITATIONS
1	Emerging Vaccine-Breakthrough SARS-CoV-2 Variants. <i>ACS Infectious Diseases</i> , 2022, 8, 546-556.	3.8	59
2	kmer2vec: A Novel Method for Comparing DNA Sequences by word2vec Embedding. <i>Journal of Computational Biology</i> , 2022, 29, 1001-1021.	1.6	8
3	Inverted repeats in coronavirus SARS-CoV-2 genome and implications in evolution. <i>Communications in Information and Systems</i> , 2021, 21, 125-145.	0.5	2
4	Analysis of SARS-CoV-2 mutations in the United States suggests presence of four substrains and novel variants. <i>Communications Biology</i> , 2021, 4, 228.	4.4	126
5	A Fast Algorithm for Computing the Fourier Spectrum of a Fractional Period. <i>Journal of Computational Biology</i> , 2021, 28, 269-282.	1.6	2
6	Latent periodicity-2 in coronavirus SARS-CoV-2 genome: Evolutionary implications. <i>Journal of Theoretical Biology</i> , 2021, 515, 110604.	1.7	0
7	UMAP-assisted K-means clustering of large-scale SARS-CoV-2 mutation datasets. <i>Computers in Biology and Medicine</i> , 2021, 131, 104264.	7.0	57
8	Inverted repeats in coronavirus SARS-CoV-2 genome manifest the evolution events. <i>Journal of Theoretical Biology</i> , 2021, 530, 110885.	1.7	2
9	Geometric construction of viral genome space and its applications. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4226-4234.	4.1	11
10	Full Chromosomal Relationships Between Populations and the Origin of Humans. <i>Frontiers in Genetics</i> , 2021, 12, 828805.	2.3	0
11	Splice sites detection using chaos game representation and neural network. <i>Genomics</i> , 2020, 112, 1847-1852.	2.9	13
12	Host Immune Response Driving SARS-CoV-2 Evolution. <i>Viruses</i> , 2020, 12, 1095.	3.3	68
13	Decoding Asymptomatic COVID-19 Infection and Transmission. <i>Journal of Physical Chemistry Letters</i> , 2020, 11, 10007-10015.	4.6	61
14	Mutations on COVID-19 diagnostic targets. <i>Genomics</i> , 2020, 112, 5204-5213.	2.9	164
15	A New Method Based on Coding Sequence Density to Cluster Bacteria. <i>Journal of Computational Biology</i> , 2020, 27, 1688-1698.	1.6	2
16	Decoding SARS-CoV-2 Transmission and Evolution and Ramifications for COVID-19 Diagnosis, Vaccine, and Medicine. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 5853-5865.	5.4	91
17	Analysis of the Hosts and Transmission Paths of SARS-CoV-2 in the COVID-19 Outbreak. <i>Genes</i> , 2020, 11, 637.	2.4	21
18	Genotyping coronavirus SARS-CoV-2: methods and implications. <i>Genomics</i> , 2020, 112, 3588-3596.	2.9	244

#	ARTICLE	IF	CITATIONS
19	Whole-genome phylogeny of giant viruses by Fourier transform. <i>Communications in Information and Systems</i> , 2020, 20, 61-76.	0.5	0
20	A Workflow to Improve Variant Calling Accuracy in Molecular Barcoded Sequencing Reads. <i>Journal of Computational Biology</i> , 2019, 26, 96-103.	1.6	0
21	Encoding and Decoding DNA Sequences by Integer Chaos Game Representation. <i>Journal of Computational Biology</i> , 2019, 26, 143-151.	1.6	13
22	Whole genome single nucleotide polymorphism genotyping of <i>Staphylococcus aureus</i> . <i>Communications in Information and Systems</i> , 2019, 19, 57-80.	0.5	1
23	A new method to cluster genomes based on cumulative Fourier power spectrum. <i>Gene</i> , 2018, 673, 239-250.	2.2	17
24	Identification of repeats in DNA sequences using nucleotide distribution uniformity. <i>Journal of Theoretical Biology</i> , 2017, 412, 138-145.	1.7	6
25	Virus Database and Online Inquiry System Based on Natural Vectors. <i>Evolutionary Bioinformatics</i> , 2017, 13, 117693431774666.	1.2	7
26	A coevolution analysis for identifying protein-protein interactions by Fourier transform. <i>PLoS ONE</i> , 2017, 12, e0174862.	2.5	20
27	Numerical encoding of DNA sequences by chaos game representation with application in similarity comparison. <i>Genomics</i> , 2016, 108, 134-142.	2.9	67
28	Periodic power spectrum with applications in detection of latent periodicities in DNA sequences. <i>Journal of Mathematical Biology</i> , 2016, 73, 1053-1079.	1.9	9
29	Virus classification in 60-dimensional protein space. <i>Molecular Phylogenetics and Evolution</i> , 2016, 99, 53-62.	2.7	31
30	Two Dimensional Yau-Hausdorff Distance with Applications on Comparison of DNA and Protein Sequences. <i>PLoS ONE</i> , 2015, 10, e0136577.	2.5	27
31	Representation of DNA sequences in genetic codon context with applications in exon and intron prediction. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1550004.	0.8	6
32	An improved model for whole genome phylogenetic analysis by Fourier transform. <i>Journal of Theoretical Biology</i> , 2015, 382, 99-110.	1.7	38
33	Ebolavirus Classification Based on Natural Vectors. <i>DNA and Cell Biology</i> , 2015, 34, 418-428.	1.9	22
34	A new method to cluster DNA sequences using Fourier power spectrum. <i>Journal of Theoretical Biology</i> , 2015, 372, 135-145.	1.7	67
35	A Novel Method for Comparative Analysis of DNA Sequences by Ramanujan-Fourier Transform. <i>Journal of Computational Biology</i> , 2014, 21, 867-879.	1.6	14
36	A measure of DNA sequence similarity by Fourier Transform with applications on hierarchical clustering. <i>Journal of Theoretical Biology</i> , 2014, 359, 18-28.	1.7	70

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37	Indian perspective Architecture for Advancement of Biomedical Telemedicine and mHealth System. Journal of Medical and Bioengineering, 2013, 2, 80-83.	0.5	0
38	A Novel Construction of Genome Space with Biological Geometry. DNA Research, 2010, 17, 155-168.	3.4	55
39	Numerical representation of DNA sequences based on genetic code context and its applications in periodicity analysis of genomes. , 2008, , .		12
40	Prediction of protein coding regions by the 3-base periodicity analysis of a DNA sequence. Journal of Theoretical Biology, 2007, 247, 687-694.	1.7	146
41	Tracking the 3-Base Periodicity of Protein-Coding Regions by the Nonlinear Tracking-Differentiator. , 2006, , .		5
42	A Fourier Characteristic of Coding Sequences: Origins and a Non-Fourier Approximation. Journal of Computational Biology, 2005, 12, 1153-1165.	1.6	81